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SEQUENCE LISTING

<110> COR Therapeutics, Inc.
Ramakrishnan, Vanitha
Phillips, David

<120> Transgenic Animals Having a Modified Glycoprotein V
Gene and Methods for Their Use

<130> 44481-5044-WO

<140> PCT/US99/17594

<141> 1999-08-04

<150> US 60/109,797

<151> 1998-08-04

<160> 14

<170> PatentIn Ver. 2.1

<210> 1

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<220>

<221> variation

<222> (13)..(18)

<223> y at position 13 = c or t; r at position 18 = a or
g.

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<213> Homo sapiens

<220>

<223> Amino acid sequence corresponding to primer of
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1

5

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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: PCR primer

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<221> variation
<222> (3)..(21)
<223> y at position 3 = c or t; r at positions 6 and 21
= a or g.

<400> 3
gayaaratgg tgytcytgga rca

23

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<212> PRT
<213> Homo sapiens

<220>
<223> Amino acid sequence corresponding to primer of
seq. id no. 7.

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Asp Lys Met Val Leu Leu Glu Gln
1 5

<210> 5
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

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<221> variation
<222> (3)..(24)
<223> y at positions 3, 12, 15, 18 and 19 = c or t; v at
position 6 = a or c or g; m at position 9 = a or
c; s at position 24 = c or g.

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ccyggvacmt tyagygayyt gatsaa

26

<210> 6
<211> 9
<212> PRT
<213> Homo sapiens

<400> 6
Pro Gly Thr Phe Ser Asp Leu Ile Lys

<210> 7
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<220>
 <221> variation
 <222> (1)..(19)
 <223> r at positions 1, 7, 10, 13, 16 and 19 = a or g;
 b at position 4 = c or g or t; k at position 6 =
 g or t.

<400> 7
 rttbckraar gergcrgcrg g

21

<210> 8
 <211> 7
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Amino acid sequence corresponding to the
 complementary strand of the primer in seq. id no.
 11.

<400> 8
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<210> 9
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

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 <221> variation
 <222> (8)..(27)
 <223> r at positions 8, 12, 15, 18, 23 and 27 = a or g;
 k at position 9 = g or t.

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 ggccccarkc crcarterca garccarga

29

<210> 10

<211> 9
<212> PRT
<213> Homo sapiens

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Ser Trp Arg Cys Asp Cys Gly Leu Gly
1 5

<210> 11
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<222> (1411)..(3108)
<223> Platelet glycoprotein V gene

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caattgccta aagttttctg acaccacaa gtgaggcact gccacatgca cccacatact 180
cctgcacagg aatgagttag tgcaatgtag catggaaaaa aaccaaagt gtggcccatg 240
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 gagccttggt tttgctcttg catttcagac atg cta aga agc gcc ctg ctg tcc 1434
 Met Leu Arg Ser Ala Leu Leu Ser

1

5

gcg gtg ctc gca ctc ttg cgt gcc caa cct ttt ccc tgc ccc aaa acc 1482
 Ala Val Leu Ala Leu Leu Arg Ala Gln Pro Phe Pro Cys Pro Lys Thr
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tgc aag tgt gtg gtc cgc gat gcc gcg cag tgc tcg ggc ggc agc gtg 1530
 Cys Lys Cys Val Val Arg Asp Ala Ala Gln Cys Ser Gly Gly Ser Val
 25 30 35 40

gct cac atc gct gag cta ggt ctg cct acg aac ctc aca cac atc ctg 1578
 Ala His Ile Ala Glu Leu Gly Leu Pro Thr Asn Leu Thr His Ile Leu
 45 50 55

ctc ttc cga atg gac cag ggc ata ttg cgg aac cac agc ttc agc ggc 1626
 Leu Phe Arg Met Asp Gln Gly Ile Leu Arg Asn His Ser Phe Ser Gly
 60 65 70

atg aca gtc ctt cag cgc ctg atg ctc tca gat agc cac att tcc gcc 1674
 Met Thr Val Leu Gln Arg Leu Met Leu Ser Asp Ser His Ile Ser Ala
 75 80 85

atc gac ccc ggc acc ttc aat gac ctg gta aaa ctg aaa acc ctc agg 1722
 Ile Asp Pro Gly Thr Phe Asn Asp Leu Val Lys Leu Lys Thr Leu Arg
 90 95 100

ttg acg cgc aac aaa atc tct cgt ctt cca cgt gcg atc ctg gat aag 1770
 Leu Thr Arg Asn Lys Ile Ser Arg Leu Pro Arg Ala Ile Leu Asp Lys
 105 110 115 120

atg gta ctc ttg gaa cag ctg ttc ttg gac cac aat gca cta agg gac 1818
 Met Val Leu Leu Glu Gln Leu Phe Leu Asp His Asn Ala Leu Arg Asp
 125 130 135

ctt gat caa aac ctg ttt cag caa ctg cgt aac ctt cag gag ctc ggt 1866
 Leu Asp Gln Asn Leu Phe Gln Gln Leu Arg Asn Leu Gln Glu Leu Gly
 140 145 150

ttg aac cag aat cag ctc tct ttt ctt cct gct aac ctt ttc tcg agc 1914
 Leu Asn Gln Asn Gln Leu Ser Phe Leu Pro Ala Asn Leu Phe Ser Ser
 155 160 165

ctg aga gaa ctg aag ttg ttg gat tta tcg cga aac aac ctg acc cac 1962
 Leu Arg Glu Leu Lys Leu Leu Asp Leu Ser Arg Asn Asn Leu Thr His

170	175	180	
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Leu Pro Lys Gly Leu Leu Gly Ala Gln Val Lys Leu Glu Lys Leu Leu			
185	190	195	200
ctc tat tca aac cag ctc acg tct gtg gat tcg ggg ctg ctg agc aac			2058
Leu Tyr Ser Asn Gln Leu Thr Ser Val Asp Ser Gly Leu Leu Ser Asn			
	205	210	215
ctg ggc gcc ctg act gag ctg cgg ctg gag cgg aat cac ctc cgc tcc			2106
Leu Gly Ala Leu Thr Glu Leu Arg Leu Glu Arg Asn His Leu Arg Ser			
	220	225	230
gta gcc ccg ggt gcc ttc gac cgc ctc gga aac ctg agc tcc ttg act			2154
Val Ala Pro Gly Ala Phe Asp Arg Leu Gly Asn Leu Ser Ser Leu Thr			
	235	240	245
cta tcc gga aac ctc ctg gag tct ctg ccg ccc gcg ctc ttc ctt cac			2202
Leu Ser Gly Asn Leu Leu Glu Ser Leu Pro Pro Ala Leu Phe Leu His			
	250	255	260
gtg agc agc gtg tct cgg ctg act ctg ttc gag aac ccc ctg gag gag			2250
Val Ser Ser Val Ser Arg Leu Thr Leu Phe Glu Asn Pro Leu Glu Glu			
	265	270	275
ctc ccg gac gtg ttg ttc ggg gag atg gcc ggc ctg cgg gag ctg tgg			2298
Leu Pro Asp Val Leu Phe Gly Glu Met Ala Gly Leu Arg Glu Leu Trp			
	285	290	295
ctg aac ggc acc cac ctg agc acg ctg ecc gcc gct gcc ttc cgc aac			2346
Leu Asn Gly Thr His Leu Ser Thr Leu Pro Ala Ala Ala Phe Arg Asn			
	300	305	310
ctg agc ggc ttg cag acg ctg ggg ctg acg cgg aac ccg cgc ctg agc			2394
Leu Ser Gly Leu Gln Thr Leu Gly Leu Thr Arg Asn Pro Arg Leu Ser			
	315	320	325
gcg ctc ccg cgc ggc gtg ttc cag ggc cta cgg gag ctg cgc gtg ctc			2442
Ala Leu Pro Arg Gly Val Phe Gln Gly Leu Arg Glu Leu Arg Val Leu			
	330	335	340
gcg ctg cac acc aac gcc ctg gcg gag ctg cgg gac gac gcg ctg cgc			2490
Ala Leu His Thr Asn Ala Leu Ala Glu Leu Arg Asp Asp Ala Leu Arg			
	345	350	355
ggc ctc ggg cac ctg cgc cag gtg tcg ctg cgc cac aac cgg ctg cgg			2538
Gly Leu Gly His Leu Arg Gln Val Ser Leu Arg His Asn Arg Leu Arg			
	365	370	375
gcc ctg ccc cgc acg ctc ttc cgc aac ctc agc agc ctc gag agc gtg			2586
Ala Leu Pro Arg Thr Leu Phe Arg Asn Leu Ser Ser Leu Glu Ser Val			
	380	385	390
cag cta gag cac aac cag ctg gag acg ctg cca gga gac gtg ttc gcg			2634
Gln Leu Glu His Asn Gln Leu Glu Thr Leu Pro Gly Asp Val Phe Ala			

0975603-020501

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tgc gac tgt ggc ctg tgg ccc ttc ctc cag tgg ctg cgg cat cac ccg Cys Asp Cys Gly Leu Trp Pro Phe Leu Gln Trp Leu Arg His His Pro 425 430 435 440			2730
gac atc ctg ggc cga gac gag ccc ccg cag tgc cgt ggc ccg gag cca Asp Ile Leu Gly Arg Asp Glu Pro Pro Gln Cys Arg Gly Pro Glu Pro 445 450 455			2778
cgc gcc agc ctg tgc ttc tgg gag ctg ctg cag ggt gac ccg tgg tgc Arg Ala Ser Leu Ser Phe Trp Glu Leu Leu Gln Gly Asp Pro Trp Cys 460 465 470			2826
ccg gat cct cgc agc ctg cct ctc gac cct cca acc gaa aat gct ctg Pro Asp Pro Arg Ser Leu Pro Leu Asp Pro Pro Thr Glu Asn Ala Leu 475 480 485			2874
gaa gcc ccg gtt ccg tcc tgg ctg cct aac agc tgg cag tcc cag acg Glu Ala Pro Val Pro Ser Trp Leu Pro Asn Ser Trp Gln Ser Gln Thr 490 495 500			2922
tgg gcc cag ctg gtg gcc agg ggt gaa agt ccc aat aac agg ctc tac Trp Ala Gln Leu Val Ala Arg Gly Glu Ser Pro Asn Asn Arg Leu Tyr 505 510 515 520			2970
tgg ggt ctt tat att ctg ctt cta gta gcc cag gcc atc ata gcc gcg Trp Gly Leu Tyr Ile Leu Leu Leu Val Ala Gln Ala Ile Ile Ala Ala 525 530 535			3018
ttc atc gtg ttt gcc atg att aaa atc ggc cag ctg ttt cga aca tta Phe Ile Val Phe Ala Met Ile Lys Ile Gly Gln Leu Phe Arg Thr Leu 540 545 550			3066
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aactaatgaa actgaccaga gcattgtgga cggggcccca aggagaatgc agtcaggatg			3168
ctggcgtgcc attacactat ttcccaggcc ttttctcctc tcccgctgctc ttagtgtctc			3228
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gttgagtaac atttgctgaa ggaacaccgg cttaaaaacga accctaggtc caagagatga			3528

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 <212> PRT
 <213> Mus musculus

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 Ala Gln Cys Ser Gly Gly Ser Val Ala His Ile Ala Glu Leu Gly Leu
 35 40 45
 Pro Thr Asn Leu Thr His Ile Leu Leu Phe Arg Met Asp Gln Gly Ile
 50 55 60
 Leu Arg Asn His Ser Phe Ser Gly Met Thr Val Leu Gln Arg Leu Met
 65 70 75 80
 Leu Ser Asp Ser His Ile Ser Ala Ile Asp Pro Gly Thr Phe Asn Asp
 85 90 95
 Leu Val Lys Leu Lys Thr Leu Arg Leu Thr Arg Asn Lys Ile Ser Arg
 100 105 110
 Leu Pro Arg Ala Ile Leu Asp Lys Met Val Leu Leu Glu Gln Leu Phe
 115 120 125
 Leu Asp His Asn Ala Leu Arg Asp Leu Asp Gln Asn Leu Phe Gln Gln
 130 135 140
 Leu Arg Asn Leu Gln Glu Leu Gly Leu Asn Gln Asn Gln Leu Ser Phe
 145 150 155 160
 Leu Pro Ala Asn Leu Phe Ser Ser Leu Arg Glu Leu Lys Leu Leu Asp
 165 170 175
 Leu Ser Arg Asn Asn Leu Thr His Leu Pro Lys Gly Leu Leu Gly Ala
 180 185 190
 Gln Val Lys Leu Glu Lys Leu Leu Leu Tyr Ser Asn Gln Leu Thr Ser
 195 200 205
 Val Asp Ser Gly Leu Leu Ser Asn Leu Gly Ala Leu Thr Glu Leu Arg
 210 215 220
 Leu Glu Arg Asn His Leu Arg Ser Val Ala Pro Gly Ala Phe Asp Arg
 225 230 235 240
 Leu Gly Asn Leu Ser Ser Leu Thr Leu Ser Gly Asn Leu Leu Glu Ser
 245 250 255

Leu Pro Pro Ala Leu Phe Leu His Val Ser Ser Val Ser Arg Leu Thr
 260 265 270
 Leu Phe Glu Asn Pro Leu Glu Glu Leu Pro Asp Val Leu Phe Gly Glu
 275 280 285
 Met Ala Gly Leu Arg Glu Leu Trp Leu Asn Gly Thr His Leu Ser Thr
 290 295 300
 Leu Pro Ala Ala Ala Phe Arg Asn Leu Ser Gly Leu Gln Thr Leu Gly
 305 310 315 320
 Leu Thr Arg Asn Pro Arg Leu Ser Ala Leu Pro Arg Gly Val Phe Gln
 325 330 335
 Gly Leu Arg Glu Leu Arg Val Leu Ala Leu His Thr Asn Ala Leu Ala
 340 345 350
 Glu Leu Arg Asp Asp Ala Leu Arg Gly Leu Gly His Leu Arg Gln Val
 355 360 365
 Ser Leu Arg His Asn Arg Leu Arg Ala Leu Pro Arg Thr Leu Phe Arg
 370 375 380
 Asn Leu Ser Ser Leu Glu Ser Val Gln Leu Glu His Asn Gln Leu Glu
 385 390 395 400
 Thr Leu Pro Gly Asp Val Phe Ala Ala Leu Pro Gln Leu Thr Gln Val
 405 410 415
 Leu Leu Gly His Asn Pro Trp Leu Cys Asp Cys Gly Leu Trp Pro Phe
 420 425 430
 Leu Gln Trp Leu Arg His His Pro Asp Ile Leu Gly Arg Asp Glu Pro
 435 440 445
 Pro Gln Cys Arg Gly Pro Glu Pro Arg Ala Ser Leu Ser Phe Trp Glu
 450 455 460
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 Asp Pro Pro Thr Glu Asn Ala Leu Glu Ala Pro Val Pro Ser Trp Leu
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 Pro Asn Ser Trp Gln Ser Gln Thr Trp Ala Gln Leu Val Ala Arg Gly
 500 505 510
 Glu Ser Pro Asn Asn Arg Leu Tyr Trp Gly Leu Tyr Ile Leu Leu Leu
 515 520 525
 Val Ala Gln Ala Ile Ile Ala Ala Phe Ile Val Phe Ala Met Ile Lys
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<213> Homo sapiens

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<221> CDS
<222> (2422)..(4101)
<223> Platelet glycoprotein V gene

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Val Leu Gln Arg Leu Met Ile Ser Asp Ser His Ile Ser Ala Val Ala	
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Pro Gly Thr Phe Ser Asp Leu Ile Lys Leu Lys Thr Leu Arg Leu Ser	
95 100 105	
cgc aac aaa atc acg cat ctt cca ggt gcg ctg ctg gat aag atg gtg	2787
Arg Asn Lys Ile Thr His Leu Pro Gly Ala Leu Leu Asp Lys Met Val	
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ctc ctg gag cag ttg ttt ttg gac cac aat gcg cta agg ggc att gac	2835
Leu Leu Glu Gln Leu Phe Leu Asp His Asn Ala Leu Arg Gly Ile Asp	
125 130 135	
caa aac atg ttt cag aaa ctg gtt aac ctg cag gag ctc gct ctg aac	2883
Gln Asn Met Phe Gln Lys Leu Val Asn Leu Gln Glu Leu Ala Leu Asn	
140 145 150	
cag aat cag ctc gat ttc ctt cct gcc agt ctc ttc acg aat ctg gag	2931
Gln Asn Gln Leu Asp Phe Leu Pro Ala Ser Leu Phe Thr Asn Leu Glu	
155 160 165 170	
aac ctg aag ttg ttg gat tta tcg gga aac aac ctg acc cac ctg ccc	2979
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Arg Asn His Leu Ala Phe Leu Pro Ser Ala Leu Phe Leu His Ser His	
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